10/532031

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FIG. 1

Human NRSF Amino Acid Sequence

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAP
QLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVGDNNFSDSEEGEGLEESADIKGE
PHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRC
DRCGYNTNRYDHYTAHLKHHTRAGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVY
TCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSSQKTHLTRHMRTHSGEKPFKC
DQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCP
VCDYAASKKCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQ
TKIKGDVAGKKNEKSVKAEKRDVSKEKKPSNNVSVIQVTTRTRKSVTEVKEMDVHTGS
NSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPKGDSKVE
ENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKG
PVQVELPPPMEHAQMEGAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVL
AHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAPMQVVQKEPVQMELSPPMEVV
QKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPP
PPREPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVS
TEDLSPPSPPLPKENLREEASGDQKLLNTGEGNKEAPLQKVGAEEADESLPGLAANIN
ESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLTGINSTVEEPVSP
MLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDS
GLHGARPVPQESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYY LEEAAQGQE

FIG. 2

Human NRSF cDNA sequence

1 ggcggcggcg gcggcgcgga ctgggtgcgc ggcgcagcgt cctgtgttgg aatgtgcggc 61 tgccgcgagc tcgcggcgca gcagcggagc gagcgccgcc gaggcccggg gccccagacc 121 ctggcggcgg ctgcggcagc cgagacggca gggcgaggcc cggaggcctg agcaccctct 181 gcagccccac tcctgggcct tcttggtcca cgacggcccc agcacccaac tttaccaccc 241 tcccccacct ctccccgaa actccagcaa caaagaaaag tagtcggaga aggagcggcg 301 actcagggtc gcccgcccct cctcaccgag gaaggccgaa tacagttatg gccacccagg 361 taatggggca gtcttctgga ggaggagggc tgtttaccag cagtggcaac attggaatgg 421 ccctgcctaa cgacatgtat gacttgcatg acctttccaa agctgaactg gccgcacctc 481 agcttattat gctggcaaat gtggccttaa ctggggaagt aaatggcagc tgctgtgatt 541 acctggtcgg tgaagaaaga cagatggcag aactgatgcc ggttggggat aacaactttt 601 cagatagtga agaaggagaa ggacttgaag agtctgctga tataaaaggt gaacctcatg 661 gactggaaaa catggaactg agaagtttgg aactcagcgt cgtagaacct cagcctgtat 721 ttgaggcatc aggtgctcca gatatttaca gttcaaataa agatcttccc cctgaaacac 781 ctggagcgga ggacaaaggc aagagctcga agaccaaacc ctttcgctgt aagccatgcc 841 aatatgaagc agaatctgaa gaacagtttg tgcatcacat cagagttcac agtgctaaga 901 aatttttgt ggaagagagt gcagagaagc aggcaaaagc cagggaatct ggctcttcca 961 ctgcagaaga gggagatttc tccaagggcc ccattcgctg tgaccgctgc ggctacaata 1021 ctaatcgata tgatcactat acagcacacc tgaaacacca caccagagct ggggataatg 1081 agcgagtcta caagtgtatc atttgcacat acacaacagt gagcgagtat cactggagga 1141 aacatttaag aaaccatttt ccaaggaaag tatacacatg tggaaaatgc aactattttt 1201 cagacagaaa aaacaattat gttcagcatg ttagaactca tacaggagaa cgcccatata 1261 aatgtgaact ttgtccttac tcaagttctc agaagactca tctaactaga catatgcgta 1321 ctcattcagg tgagaagcca tttaaatgtg atcagtgcag ttatgtggcc tctaatcaac 1381 atgaagtaac ccgccatgca agacaggttc acaatgggcc taaacctctt aattgcccac 1441 actgtgatta caaaacagca gatagaagca acttcaaaaa acatgtagag ctacatgtga 1501 acccacggca gttcaattgc cctgtatgtg actatgcagc ttccaagaag tgtaatctac 1561 agtatcactt caaatctaag catcctactt gtcctaataa aacaatggat gtctcaaaag 1621 tgaaactaaa gaaaaccaaa aaacgagagg ctgacttgcc tgataatatt accaatgaaa 1681 aaacagaaat agaacaaaca aaaataaaag gggatgtggc tggaaagaaa aatgaaaagt 1741 ccgtcaaagc agagaaaaga gatgtctcaa aagagaaaaa gccttctaat aatgtgtcag 1801 tgatccaggt gactaccaga actcgaaaat cagtaacaga ggtgaaagag atggatgtgc 1861 atacaggaag caattcagaa aaattcagta aaactaagaa aagcaaaagg aagctggaag 1921 ttgacagcca ttctttacat ggtcctgtga atgatgagga atcttcaaca aaaaagaaaa 1981 agaaggtaga aagcaaatcc aaaaataata gtcaggaagt gccaaagggt gacagcaaag 2041 tggaggagaa taaaaagcaa aatacttgca tgaaaaaaag tacaaagaag aaaactctga 2101 aaaataaatc aagtaagaaa agcagtaagc ctcctcagaa ggaacctgtt gagaagggat 2161 ctgctcagat ggaccctcct cagatggggc ctgctcccac agaggcggtt cagaaggggc 2221 ccgttcaggt ggagctgcca cctcccatgg agcatgctca gatggagggt gcccagatac 2281 ggcctgctcc tgacgagcct gttcagatgg aggtggttca ggaggggcct gctcagaagg 2341 agctgctgcc tcccgtggag cctgctcaga tggtgggtgc ccaaattgta cttgctcaca 2401 tggagctgcc tcctcccatg gagactgctc agacggaggt tgcccaaatg gggcctgctc 2461 ccatggaacc tgctcagatg gaggttgccc aggtagaatc tgctcccatg caggtggtcc 2521 agaaggagcc tgttcagatg gagctgtctc ctcccatgga ggtggtccag aaggagcctg 2581 ttcagataga gctgtctcct cccatggagg tggtccagaa ggaacctgtt aagatagagc 2641 tgtctcctcc catagaggtg gtccagaagg agcctgttca gatggagttg tctcctccca 2701 tgggggtggt tcagaaggag cctgctcaga gggagccacc tcctcccaga gagcctcccc 2761 ttcacatgga gccaatttcc aaaaagcctc ctctccgaaa agataaaaag gaaaagtcta 2821 acatgcagag tgaaagggca cggaaggagc aagtccttat tgaagttggc ttagtgcctg 2881 ttaaagatag ctggcttcta aaggaaagtg taagcacaga ggatctctca ccaccatcac 2941 caccactgcc aaaggaaaat ttaagagaag aggcatcagg agaccaaaaa ttactcaaca 3001 caggtgaagg aaataaagaa gcccctcttc agaaagtagg agcagaagag gcagatgaga 3061 gcctacctgg tcttgctgct aatatcaacg aatctaccca tatttcatcc tctggacaaa 3121 acttgaatac gccagagggt gaaactttaa atggtaaaca tcagactgac agtatagttt 3181 gtgaaatgaa aatggacact gatcagaaca caagagagaa tctcactggt ataaattcaa 3241 cagttgaaga accagtttca ccaatgcttc ccccttcagc agtagaagaa cgtgaagcag 3301 tgtccaaaac tgcactggca tcacctcctg ctacaatggc agcaaatgag tctcaggaaa 3361 ttgatgaaga tgaaggcatc cacagccatg aaggaagtga cctaagtgac aacatgtcag 3421 agggtagtga tgattctgga ttgcatgggg ctcggccagt tccacaagaa tctagcagaa 3481 aaaatgcaaa ggaagccttg gcagtcaaag cggctaaggg agattttgtt tgtatcttct 3541 gtgatcgttc tttcagaaag ggaaaagatt acagcaaaca cctcaatcgc catttggtta 3601 atgtgtacta tcttgaagaa gcagctcaag ggcaggagta atgaaacttt gaacaaggtt 3661 tca

FIG. 3

Mouse NRSF Amino Acid Sequence

MATQVMGQSSGGGSLFNNSANMGMALTNDMYDLHELSKAELAAP
QLIMLANVALTGEASGSCCDYLVGEERQMAELMPVGDNHFSESEGEGLEESADLKGLE
NMELGSLELSAVEPQPVFEASAAPEIYSANKDPAPETPVAEDKCRSSKAKPFRCKPCQ
YEAESEEQFVHHIRIHSAKKFFVEESAEKQAKAWESGSSPAEEGEFSKGPIRCDRCGY
NTNRYDHYMAHLKHHLRAGENERIYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCSKC
NYFSDRKNNYVQHVRTHTGERPYKCELCPYSSSQKTHLTRHMRTHSGEKPFKCDQCNY
VASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYA
ASKKCNLQYHFKSKHPTCPSKRMDVSKVKLKKTKKREADLLNNAVSNEKMENEQTKTK
GDVSGKKNEKPVKAVGKDASKEKKPGSSVSVVQVSTRTRKSAVAAETKAAEVKHTDGQ
TGNNPEKPCKAKKNKRKKDAEAHPSEEPVNEGPVTKKKKKSECKSKISTNVPKGGGRA
EERPGVKKQSASLKKGTNKTPPKTKTSKKGGKLAPKGMGQTEPSSGALAQVGVSPDPA
LIQAEVTGSGSSQTELPSPMDIAKSEPAQMEVSLTGPPPVEPAQMEPSPAKPPQVEAP
TYPQPPQRGPAPPTGPAPPTGPAPPTEPAPPTGLAEMEPSPTEPSQKEPPPSMEPPCP
EELPQAEPPPMEDCQKELPSPVEPAQIEVAQTAPTQVQEEPPPVSEPPRVKPTKRSSL
RKDRAEKELSLLSEMARQEQVLMGVGLVPVRDSKLLKGNKSAQDPPAPPSPSPKGNSR
EETPKDQEMVSDGEGTIVFPLKKGGPEEAGESPAELAALKESARVSSSEQNSAMPEGG
ASHSKCQTGSSGLCDVDTEQKTDTVPMKDSAAEPVSPPTPTVDRDAGSPAVVASPPIT
LAENESQEIDEDEGIHSHDGSDLSDNMSEGSDDSGLHGARPTPPEATSKNGKAGLAGK
VTEGEFVCIFCDRSFRKEKDYSKHLNRHLVNVYFLEEAAEEQEEQEEREEQE

FIG. 4

Mouse NRSF cDNA

atggccaccc aggtgatggg gcagtcttct ggaggaggca gtctcttcaa caacagtgcc 61 aacatgggca tggccttaac caacgacatg tacgacctgc acgagctctc gaaagctgaa 121
ctggcagccc ctcagctcat catgttagcc aacgtggccc tgacggggga ggcaagcggc 181 agctgctgcg attacctggt cggtgaagag aggcagatgg ccgaattgat gcccgtggga 241
gacaaccact tctcagaaag tgaaggagaa ggcctggaag agtcggctga cctcaaaggg 301 ctggaaaaca tggaactggg aagtttggag ctaagtgctg tagaacccca gcccgtattt 361
gaagcctcag ctgccccaga aatatacagc gccaataaag atcccgctcc agaaacaccc 421 gtggcggaag acaaatgcag gagttctaag gccaagccct tccggtgtaa gccttgccag 481
tacgaagccg aatctgaaga gcagtttgtg catcacatcc ggattcacag cgctaagaag 541 ttctttgtgg aggaaagtgc agagaaacag gccaaagcct gggagtcggg gtcgtctccg 601
gccgaagagg gcgagttctc caaaggcccc atccgctgtg accgctgtgg atacaatacc 661 aaccggtatg accactacat ggcacacctg aagcaccacc tgcgagctgg cgagaacgag 721
cgcatctaca agtgcatcat ctgcacgtac acgacggtca gcgagtacca ctggaggaaa 781 cacctgagaa accatttccc caggaaagtc tacacctgca gcaagtgcaa ctacttctca 841
gacagaaaaa ataactacgt tcagcacgtg cgaactcaca caggagaacg cccgtataaa 901 tgtgaacttt gtccttactc aagctctcag aagactcatc taacgcgaca catgcggact 961
cattcaggtg agaagccatt taaatgtgat cagtgcaatt atgtggcctc taatcagcat 1021 gaagtgaccc gacatgcaag acaggttcac aacgggccta aacctcttaa ttgcccgcac 1081
tgtgactaca aaacagcaga tagaagcaac ttcaaaaagc acgtggagct gcatgttaac 1141 ccacggcagt tcaactgccc cgtgtgtgac tacgcggctt ctaagaagtg taatctacaa 1201
taccatttca aatctaagca tcccacctgt cccagcaaaa gaatggatgt ctccaaagtg 1261 aagctaaaga aaaccaaaaa gagagaggct gacctgctta ataacgccgt cagcaacgag 1321
aagatggaga atgagcaaac aaaaacaaag ggggatgtgt ctgggaagaa gaacgagaaa 1381 cctgtaaaag ctgtgggaaa agatgcttca aaagagaaga agcctggtag cagtgtctca 1441
gtggtccagg taagtaccag gactcggaag tcagcggtgg cggcggagac taaagcagca 1501 gaggtgaaac acacagacgg acaaacagga aacaatccag aaaagccctg taaagccaag 1561 aaaaacaaaa gaaagaagga tgctgaggcc catccctccg aagagcctgt gaacgaggga 1621 ccagtgacaa aaaagaaaaa gaagtctgag tgcaaatcaa aaatcagtac caacgtgcca 1681 aagggcggcg gccgagcgga ggagaggccg ggggtcaaga agcaaagcgc ttcccttaag 1741 aaaggcacaa ataagacgcc gcccaagaca aagacaagta aaaaaggtgg caaacttgct 1801 ccaaagggga tggggcagac agaaccttct tctggggcat tggctcaagt gggggtgtct 1861 ccagaccctg ccctcattca ggcagaggtc accgggtcag gatcttctca gacagagctt 1921 ccttcaccca tggatattgc taagtcagag cccgcccaga tggaggtttc cctaacaggg 1981 ccacctccgg tggagcctgc tcaaatggag ccatcgcctg cgaaacctcc ccaggtagaa 2041 gcacccactt acccccagcc tccccaaagg gggcctgccc ctcccacggg gcctgcccct 2101 cccacggggc ctgcccctcc cacggagcct gcccctccca cggggcttgc cgagatggaa 2161 ccttctccca cggagccttc ccagaaggaa ccacctccca gtatggagcc tccctgcccc 2221 gaggagctgc ctcaggccga gccacctcct atggaggatt gtcagaagga gctgccttct 2281 cccgtggagc ccgctcagat tgaggttgct cagacggccc ctacgcaggt tcaggaggag 2341 ccccctcctg tctcggagcc acctcgggtg aagccaacca aaagatcatc tctccggaaa 2401 gacagagcag agaaggagct gagcctgctg agtgagatgg cgcggcagga gcaggtcctc 2461 atgggggttg gcttggtgcc tgttagagac agcaagcttc tgaagggaaa caagagcgcc 2521 caggacccca cagccccacc gtcaccatcg ccaaagggaa actcgaggga agagacaccc 2581 aaggaccaag aaatggtctc tgatggggaa ggaactatag tattccctct caagaaagga 2641 ggaccagagg aagctggaga gagtccagct gagttggctg ctctcaagga gtctgcccgt 2701 gtttcatcct ctgaacaaaa ctcagccatg ccagagggtg gagcatcaca cagcaagtgt 2761 cagactggct cctctgggct ttgtgacgtg gacactgagc agaagacaga tactgtcccc 2821 atgaaagact ccgcagcaga gccagtgtcc cctcctaccc caacagtgga ccgtgacgca 2881 gggtcaccag ctgtagtggc ctcccctcct atcacgttgg ctgaaaacga gtctcaggaa 2941 attgatgaag atgaaggcat ccatagccat gatggaagtg acctgagtga caacatgtct 3001 gaggggagtg acgactcagg actgcacggg gctcggccga caccaccaga agctacgtca 3061 aaaaatggga aggcagggtt ggctggtaaa gtgactgagg gagagtttgt gtgtattttc 3121 tgtgatcgtt cttttagaaa ggaaaaagat tatagcaaac acctcaatcg ccacttggtg 3181 aatgtgtact tcctagaaga agcagctgag gagcaggagg agcaggagga gcgggaggag 3241 caggagtag

FIG. 5

Rat NRSF Amino Acid Sequence

MATQVMGQSSGGGSLFNNSGNMGMALPNDMYDLHDLSKAELAAP
QLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVGDNHFSDSEGEGLEESAELKGDP
SGLDNMELRSLELSVVEPQPVFEASAAPEVYSSNKDPAPEAPVAEDKCKNLKAKPFRC
KPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGASPSEEGEFSKGPIRCD
RCGYNTNRYDHYTAHLKHHLRAGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYT
CSKCNYFSTEKNNYVQHVRTHTGERPYKCELCPYSSSQKTHLTRHMRTHSGEKPFKCD
QCNYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPV
CDYAASKKCNLQYHFKSKHPTCPSKTMDVSKVKLKKTKRREADLHRDAAAAATEQTDT
EQAKTKGVDASARRSERPVKGVGKDVPKEKKPCSNASVVQVTTRTRKSAVETKAAEGK
HTDGQTGNNAEKSSKAKKSKRKMDAEAHPSVEPVTEGPVTKKKKTESKPKTSGEVPKG
SRVEDRKADKQQSASIKKGGKKTALKTKTAKKGSKLAPKWVGHTEPSSEMAQGGESPV
PALTQAVVTPSGSTQTELSSPMDIAQTEPAQMDVSQTGPPQVQRPLPVEPAQLEPSPP
QEPPQVEPPACVEPPPPVEPPCPMEPAEMEPSPPMEPSQVEPPPHLEPPLPMELPQVE
LPPVEDCQKELPPVEHAQTKVAQTGPTQVGAVQEEPLFCLRATSSQANQKVISPKDRA
KEKLSVLSEMARQEQVLIEVGLVPVRDSQLLKASKSAPDLPAPPSPLPKGHLRREETP
KDQEMFSDGEGNKVSPLEKGGTEEAGESRAELAAPMESTSALSSEQSSNAPDGETLHS
ECQADSTAVCEMEVDTEQKTDRVPLKDSAVEPVSPLNPRVDPEAAAPAVVASPPITLA
ESQEIDEDEGIHSHDGSDLSDNMSEGSDDSGLHGARPAPQEATSKSGKEGLAVKVTEG
EFVCIFCDRSFRKEKDYSKHLNRHLVNVYFLEEAAEEQ

FIG. 6

Rat NRSF cDNA Sequence

atggccaccc aggtgatggg gcagtcttct ggaggaggaa gtctctttaa caacagtggc 61 aacatgggca tggccttacc caacgacatg tatgacttgc acgacctctc gaaagctgaa 121
ctggcggcac ctcagctcat tatgttagcc aacgtggccc tgactgggga agtgaatggc 181 agctgctgtg attacctggt tggtgaagag agacagatgg ccgagttgat gcctgttgga
241 gacaaccact tttcagatag cgaaggagaa ggccttgagg agtcggctga actaaaaggt 301 gaccccagtg ggctggacaa catggaactg agaagtttgg agctaagcgt
tgtagagccc 361 cagcccgtat ttgaagcatc agctgcccca gaagtgtaca gctcgaataa agatcccgcc 421 cctgaagcac ccgtggcgga ggacaaatgc aagaatttga
aggccaaacc cttccgttgt 481 aagccatgcc agtatgaagc ggagtctgaa gaacagttcg tacatcacat ccgggttcac 541 agtgctaaga agtttttgt ggaagagagt
gcagagaagc aagccaaagc cagggaatct 601 ggggcttccc cgtctgagga gggcgagttc tccaagggtc ccatccgctg tgatcgctgt 661 ggctacaata ccaaccggta
tgatcactac acggcacacc tgaagcacca cctgagagcc 721 ggggataacg agcgtgtcta caagtgtatc atttgcacgt acacgacagt cagcgaatac 781 cactggcgga
aacacctgag gaaccatttt cccaggaaag tctacacgtg tagcaagtgc 841 aactattttt cgacagaaaa aaataattat gttcaacacg ttcgaactca cacaggagaa 901 cgcccttata
aatgtgaact gtgtccttac tcaagttctc agaagactca tctaactcga 961 cacatgcgta ctcactcagg tgagaagcca tttaaatgtg atcagtgcaa ttatgtggcc 1021 tctaatcagc
acgaagtgac ccgacacgca agacaggttc acaacgggcc taaacctctt 1081 aattgccctc actgtgacta caaaacagcc gataggagca acttcaagaa gcacgtcgag 1141
ctgcacgtca accctcggca gttcaactgc cccgtgtgtg actacgcggc ctccaagaag 1201 tgtaacctgc agtaccattt caagtccaag caccccacct gccccagcaa gacgatggac
1261 gtgtccaaag tgaagctgaa gaaaaccaag aggagggagg ctgacctgca ccgtgacgcc 1321 gccgccgccg ccactgagca gacggacaca gagcaagcga aaaccaaggg
ggtggacgcg 1381 tctgcgagga gaagtgagag gcctgtaaaa ggcgttggaa aagatgttcc aaaagagaag 1441 aagccctgta gcaatgcctc tgtggtgcag gtaactaccc
gaactcggaa atcagcggtg 1501 gagactaaag cagcggaggg aaaacacaca gatggacaga caggaaacaa cgcagaaaag 1561 tcctctaaag ctaagaagag caaaaggaag
atggacgccg aggcccatcc ctcggtcgag 1621 cctgtgactg agggacccgt gacaaagaag aaaaagacgg agagcaaacc caagaccagc 1681 ggcgaagtgc cgaagggcag
cagagtggag gacaggaagg cggacaaaca gcaaagtgct 1741 tccattaaga aaggcgggaa gaagacggct ctcaagacta agacagctaa aaaaggcagc 1801 aaacttgctc
cgaagtgggt ggggcacaca gaaccttcct cggagatggc tcaaggaggg 1861 gagtctccag ttcctgctct cactcaggcg gtggtcaccc catcaggatc tactcagaca 1921
gagctctctt ctcccatgga tattgctcag acagagcctg cccagatgga cgtttcccag 1981 acagggccgc ctcaggtgca gcggcctctt cctgtggagc ctgctcaatt ggagccgtct
2041 cctcctcagg agcctcccca ggtagagcca cctgcctgtg tggagcctcc ccctcccgtg 2101 gagcctccat gtcccatgga gcctgctgag atggaaccgt cccctcccat
ggagccttcc 2161 caggtggagc cacctcctca tttggagcct ccgcttccca tggagctgcc tcaggtggag 2221 ctgcctcctg tggaggattg tcagaaggag ctgcctcctg
tggagcatgc tcagactaag 2281 gttgctcaga caggtcctac tcaggtggga gctgttcagg aggagccccc tttctgtctc 2341 cgagccacct caagtcaagc taaccagaag
gtcatctccc cgaaagaccg tgccaaggag 2401 aagttgagcg tgctgagtga gatggcgagg caggagcagg ttcttattga ggttggctta 2461 gtgcctgtca gagatagcca
gcttctgaag gccagcaaga gcgcaccgga cctcccagcc 2521 ccaccgtcac cactgccaaa gggacacttg agaagagaag agacacccaa ggaccaagaa 2581 atgttctctg
acggggaagg aaataaagta tcccctctcg agaaaggagg aacagaggaa 2641 gctggtgaga gtcgagctga gctggctgct cccatggaat ctaccagtgc tttatcctct 2701
gaacaaagct caaatgcacc agatggtgaa acattacaca gcgagtgtca ggctgactcc 2761 actgcggttt gtgaaatgga agtggacact gagcagaaga cagaccgtgt ccctctgaaa
2821 gactcagcag tagaaccagt gtcacctctt aacccaagag tggaccctga agcagcggca 2881 ccagctgtgg tggcctcccc tcctatcact ttggccgagt ctcaggaaat
tgatgaggat 2941 gaaggcattc acagccatga tggaagtgac ctgagcgaca acatgtctga ggggagtgat 3001 gactcaggac tgcatggggc tcggccagca ccacaggaag
ctacgtcaaa aagtggaaag 3061 gaagggttgg ctgtcaaagt aactgaggga gagtttgttt gtatttttg tgatcgttct 3121 tttagaaagg aaaaagacta tagcaaacac ctcaatcgcc
atttggttaa tgtgtacttc 3181 cttgaagaag cagctgagga gcaggagtag agtagctgat cctcgaggag aagcgcaatg 3241 cgactttgta a

FIG. 7

Xenopus NRSF partial Amino Acid Sequence

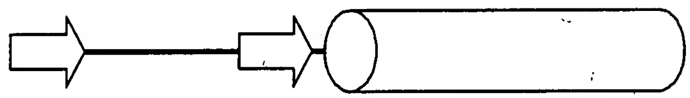
MATQMVNQSTGNSLFCTSTYSNISLDNDMYGLHDLSKADMAAPR
LIMLANVALTGELSSGCCDYTPEGERQMAELTTVNDNSFSDSEGDRLEDSPSMDIQSH
NFIMEMEPAECSKEGTSENDGTLLSNTLEVEVQKDKRTPSPTDDKYKCVKSKPFRCKP
CQYKAESEEEFVHHIKIHSAKIYVDNDSNKKAQGNEADSSISEESDVSKGPIQCDRCG
YNTNRFDHYLAHLKHHNKAGENERVYKCTICTYTTVSEYHWKKHLRNHYPRILYTCSQ
CSYFSDRKNNYIQHIRTHTGERPYQCILCPYSSSQKTHLTRHMRTHSGEKPFKCEQCS
YVASNQHEVTRHARQVHNGPKPLTCPHCDYKTADRSNFKKHVELHVNPRQFLCPVCDY
AASKKCNLQYHIKSRHSGCTNITMDVSKVKLRTKKGDIGVADVDANKQTENGNIIDKS
VEETVKAEKRESCGKAKKSIVNLVDGQVAKKRRLSSTQKKIKTSDARPEKILDKSRKS
SCVKRKSDLLENSNDTQTSTV

FIG. 8

Xenopus NRSF partial cDNA sequence

```
   1 ggcacgagca gtcggttgag acgccgattt gagaaccgtg gacagttctt gaatttggga
  61 gggagaatgg cgcaagtgtg cgaccggatt cccgaaaagt tataaacatg gccactcaaa
 121 tggtcaacca gtctacaggt aacagcttgt tctgtaccag cacctactcc aatatttcat
 181 tggacaatga catgtatggg ttgcatgacc tttcaaaagc tgatatggca gcccctcgat
 241 tgataatgct agcaaatgtg gctctgactg gcgaactcag tagtggttgc tgtgattaca
 301 cgccagaagg agaaaggcaa atggcagaac taacaactgt aaatgacaac agcttctcag
 361 atagtgaggg ggataggttg gaagattcac ccagcatgga tattcagtca cacaatttta
 421 taatggagat ggagccagct gaatgttcaa aagaaggaac gtctgaaaat gatggaactc
 481 tactctctaa tacacttgag gtggaggttc aaaaggataa aaggacaccc agcccaacag
 541 atgacaaata caaatgtgtg aaaagcaaac catttcggtg caaaccttgt cagtacaaag
 601 cagagtctga agaagaattt gttcatcaca ttaagattca cagcgctaag atatatgttg
 661 ataatgactc aaataaaaaa gcgcagggta atgaggcaga ttctagcata tcggaggaat
 721 ctgatgtctc caaaggacct attcagtgtg acaggtgtgg atacaataca aatcgttttg
 781 atcactatct ggctcattta aagcatcaca acaaagctgg agaaaatgaa agagtataca
 841 aatgtacaat atgtacttat actacagtca gtgaatatca ctggaagaaa catctacgta
 901 accattatcc aaggatactc tatacatgct cacaatgttc ctatttttct gataggaaaa
 961 ataattatat ccagcatata agaacacata caggagaacg accatatcag tgtattctat
1021 gtccttactc aagctcacag aaaacccact tgaccaggca catgcgaact cattcaggtg
1081 agaagccttt caaatgtgag cagtgtagtt atgttgcatc caatcagcat gaagttacac
1141 gtcatgcaag acaggttcac aatggaccaa aaccattaac ttgccctcat tgtgactaca
1201 aaactgcaga tcgcagtaat ttcaagaagc atgtagagtt acatgttaat cctcgacagt
1261 ttctatgccc tgtttgtgac tatgctgctt ccaaaaagtg taacttgcaa tatcatataa
1321 aatccagaca ctcaggatgc acaaatatca caatggatgt ttccaaagta aaactgagga
1381 caaagaaagg agacatagga gttgcagatg ttgatgcaaa taagcaaaca gagaatggaa
1441 atataataga taaatctgtg gaagagaccg ttaaagcaga gaaaagggaa agctgtggga
1501 aagctaaaaa aagtattgtt aatttagttg atggccaggt tgcaaaaaaa aggcgcttgt
1561 catctactca gaaaaaaatt aaaacttcag acgcaaggcc tgaaaagatt ttagataaat
1621 cccgtaagtc tagttgtgtg aaaagaaaat ctgatttatt agaaaattct aatgataccc
1681 aaacaagcac tgtg
```

FIG. 9



Zif268	RPYA	**C**	PVES	**C**	DRRFS	RSDELTR	**H**	IRI -	**H**	TGQK P
	FQ	**C**	RI --	**C**	MRNFS	RSDHLTT	**H**	IRT -	**H**	TGEK P
	FA	**C**	DI --	**C**	GRKFA	RSDERKR	**H**	TKI -	**H**	LRQKD
NRSF	KPFR	**C**	KP --	**C**	Q**Y**EAE	SEEQFVH	**H**	IRV -	**H**	SAKKFFVEESAEKQAKARESGSSTAEEGDFSKGP
	IR	**C**	DR --	**C**	G**Y**NTN	RYDHYTA	**H**	LKH -	**H**	TRAGDNERV
	YK	**C**	II --	**C**	T**Y**TTV	SEYHWRK	**H**	LRN -	**H**	FPRKV
	YT	**C**	GK --	**C**	N**Y**FSD	RKNNYVQ	**H**	VRT -	**H**	TGERP
	YK	**C**	EL --	**C**	P**Y**SSS	QKTHLTR	**H**	MRT -	**H**	SGEKP
	FK	**C**	DQ --	**C**	S**Y**VAS	NQHEVTR	**H**	ARQV	**H**	NGPKP
	LN	**C**	PH --	**C**	D**Y**KTA	DRSNFKK	**H**	VEL -	**H**	VNPRQ
	FN	**C**	PV --	**C**	D**Y**AAS	KKCNLQY	**H**	FKSK	**H**	PTCPN

FIG. 10

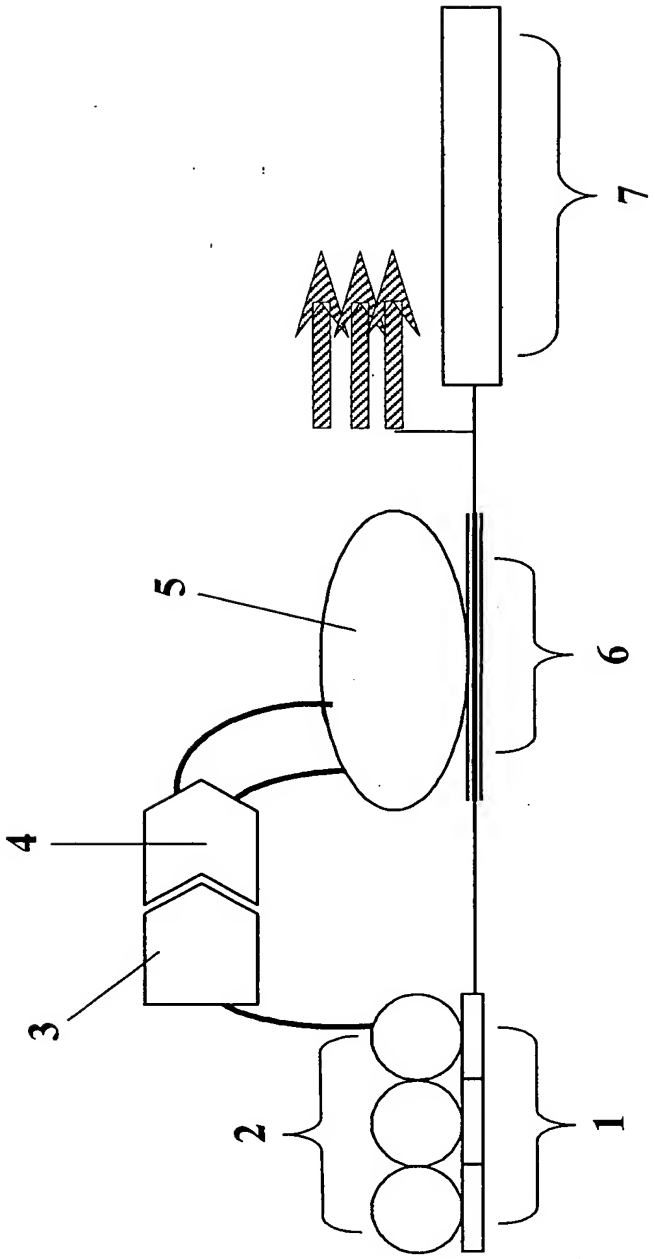


FIG. 11

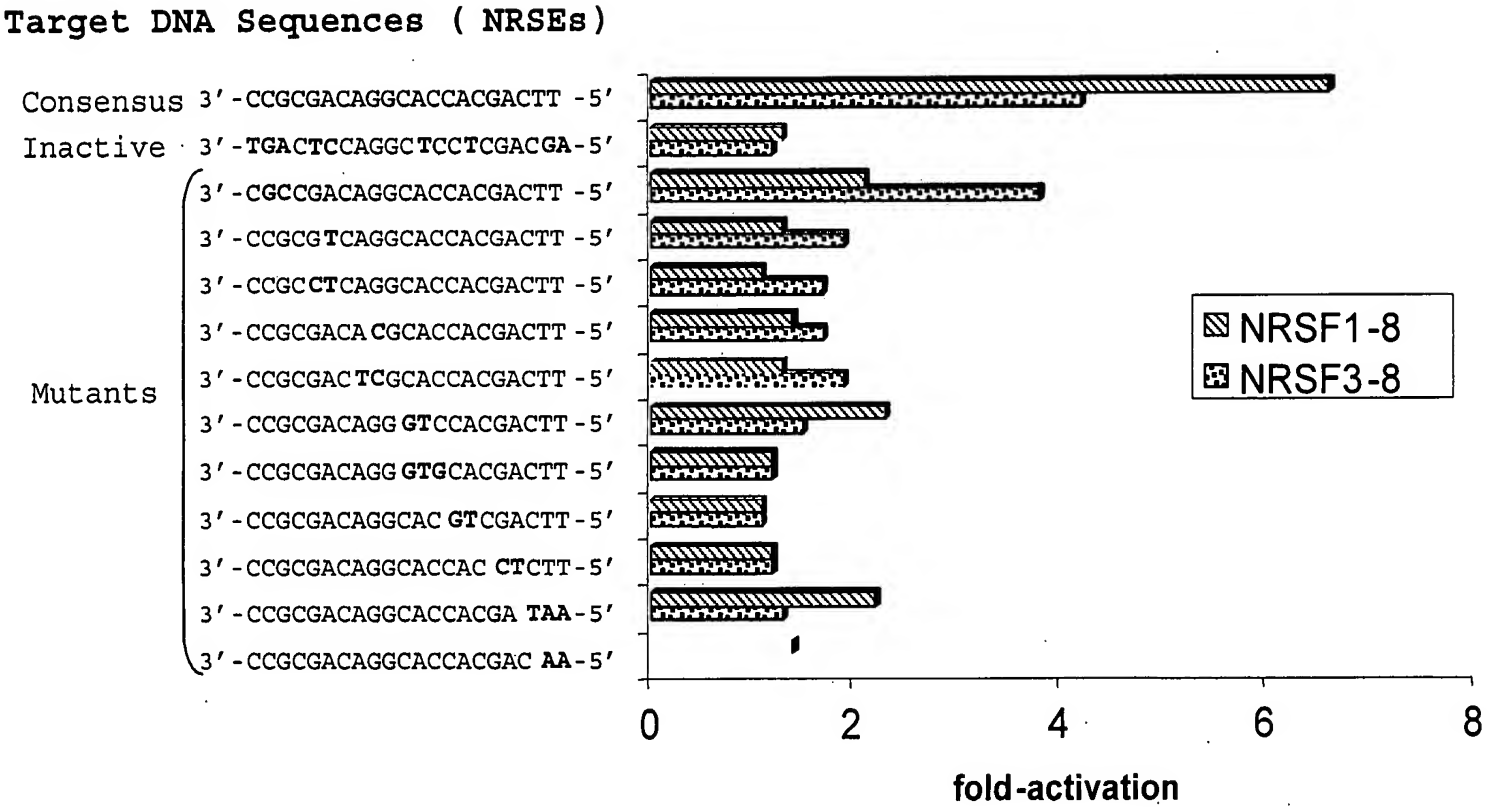


FIG. 12

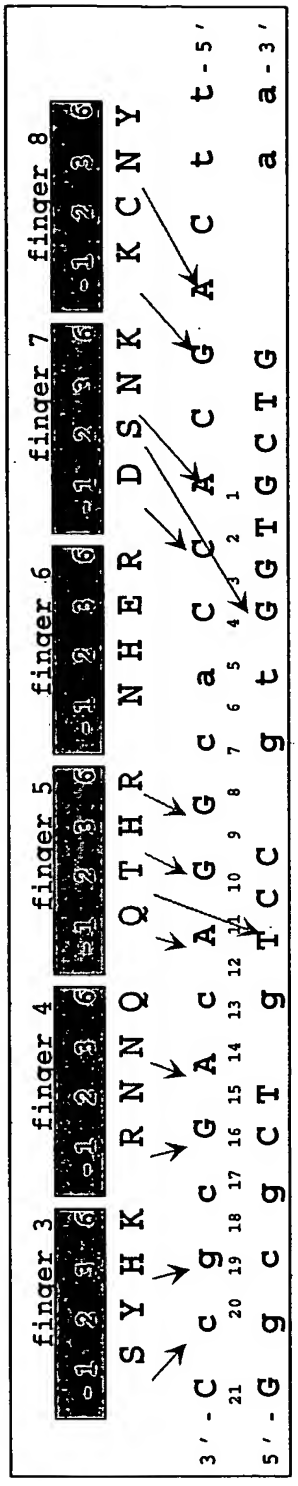

finger 3
finger 4
finger 5
finger 6
finger 7
finger 8
S Y H K R N N Q Q T H R N H E R D S N K K C N Y
3′-C c g c g A c G G G c a C C A C G A C t t-5′
5′-G g c g C T g T C C g t G G T G C T G a a-3′

FIG. 13

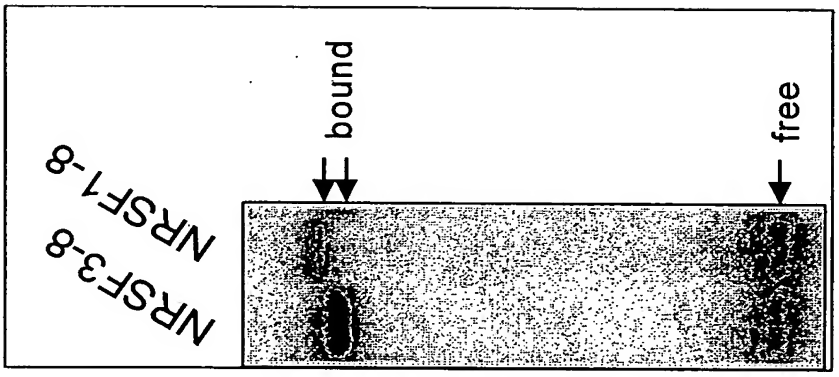


FIG. 14

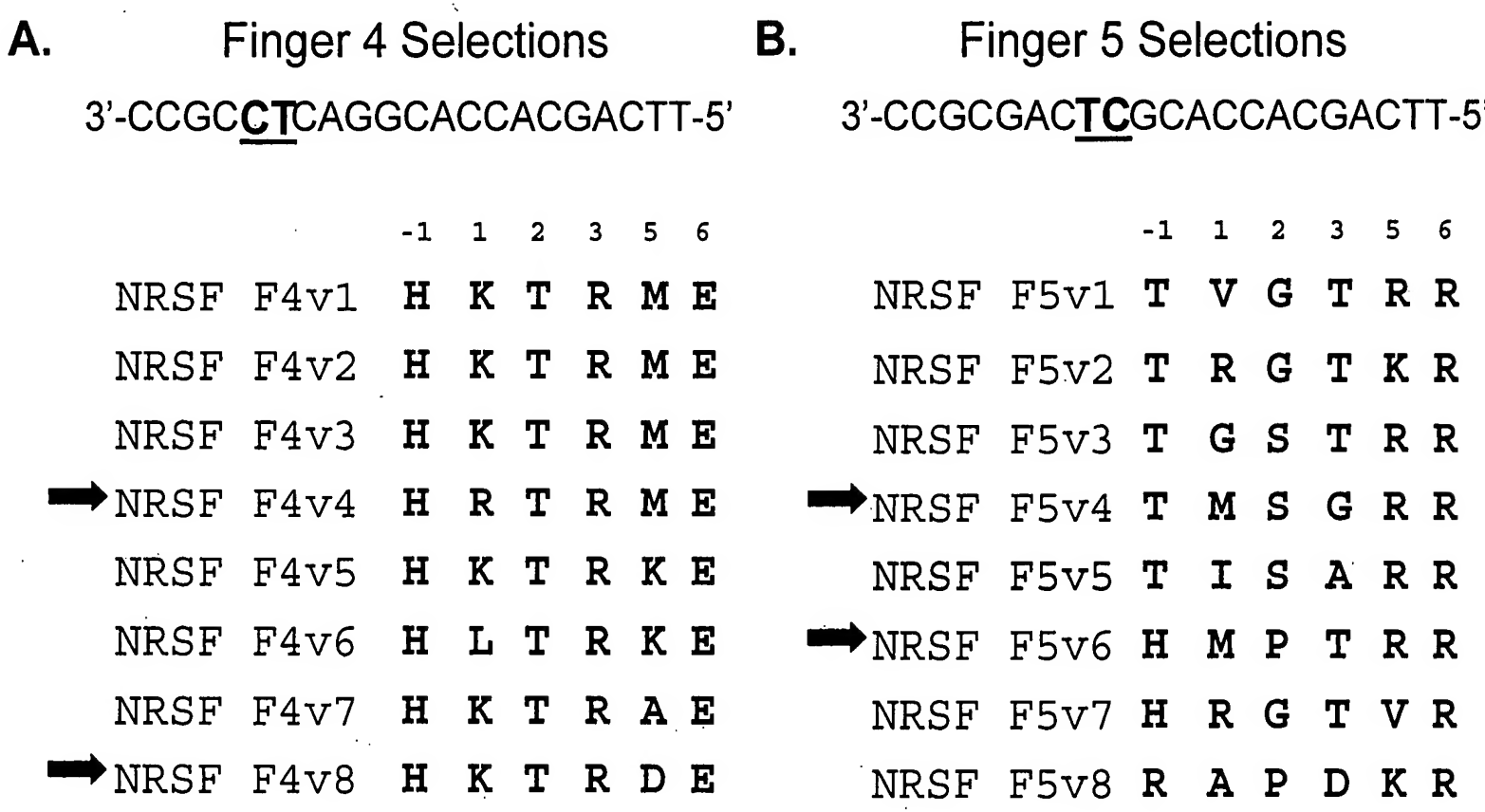


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FIG. 15A

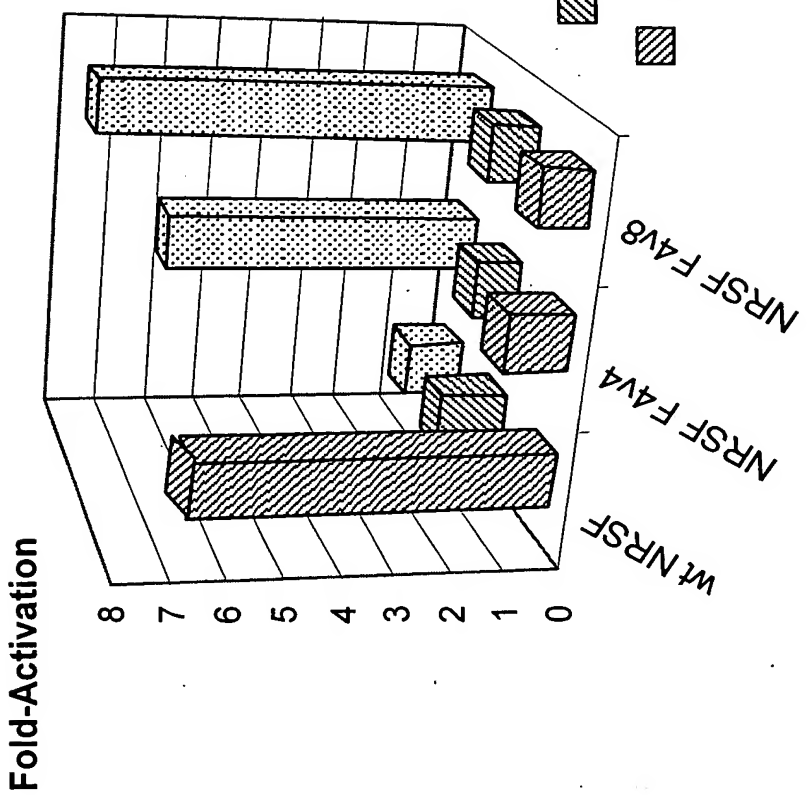

Fold-Activation
0
1
2
3
4
5
6
7
8
wt NRSF
NRSF F4v4
NRSF F4v8
3'- CCGCCT CAGGCACCACGACTT-5'
(Target double mutant NRSE)
3'- CCGCGT CAGGCACCACGACTT-5'
(Single mutant NRSE)
3'- CCGCGACAGGCACCACGACTT-5'
(Consensus NRSE)

FIG. 15B

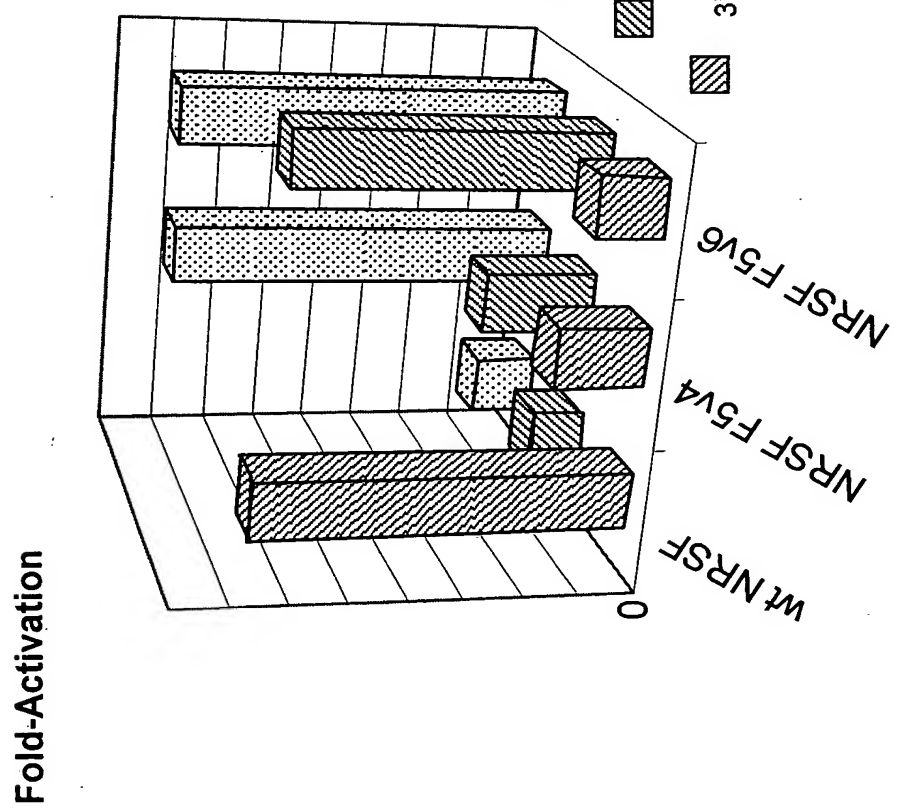

Fold-Activation
0
wt NRSF
NRSF F5v4
NRSF F5v6
3'- CCGCGACTC GCACCACGACTT-5'
(Target double mutated NRSE)
3'- CCGCGACAC GCACCACGACTT-5'
(Single mutant NRSE)
3'- CCGCGACAGGCACCACGACTT-5'
(Consensus NRSE)

FIG. 16

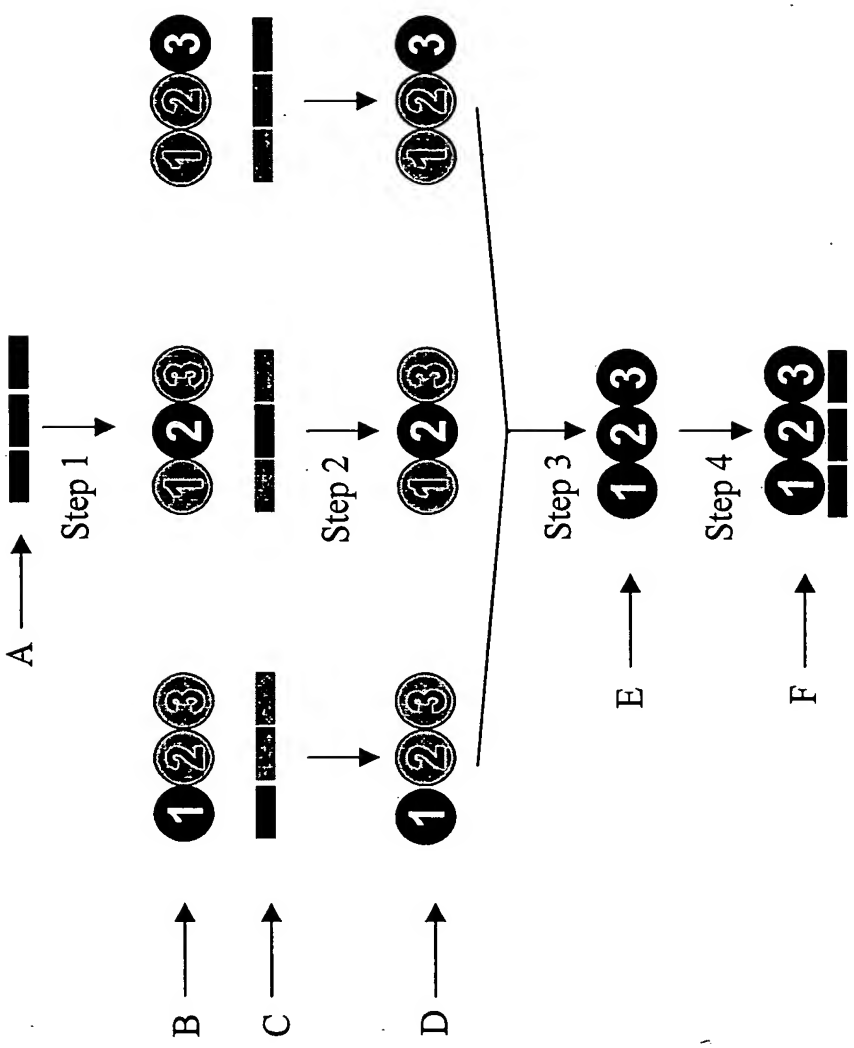


FIG. 17

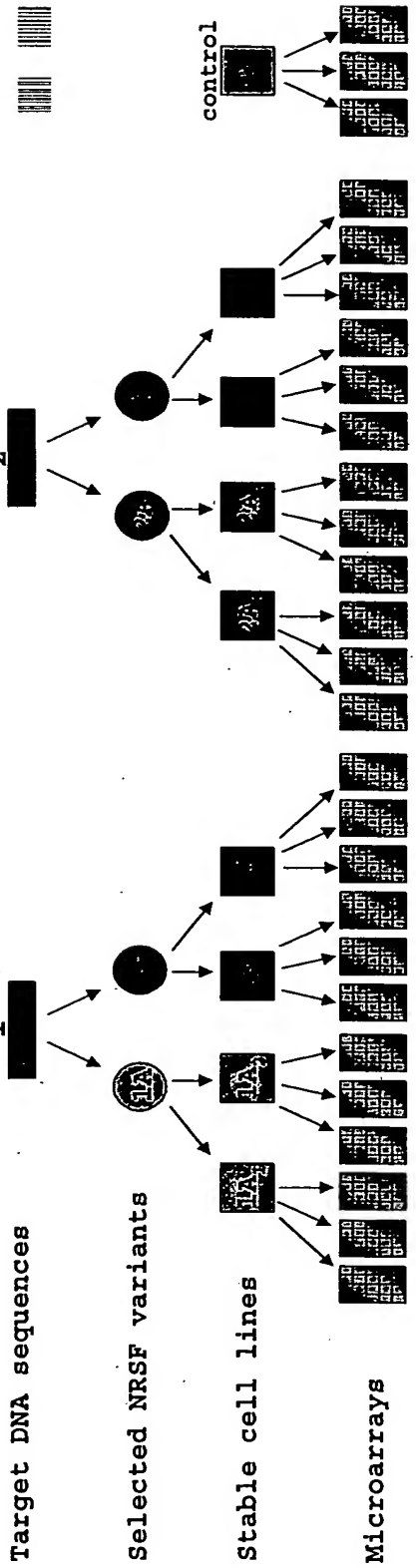
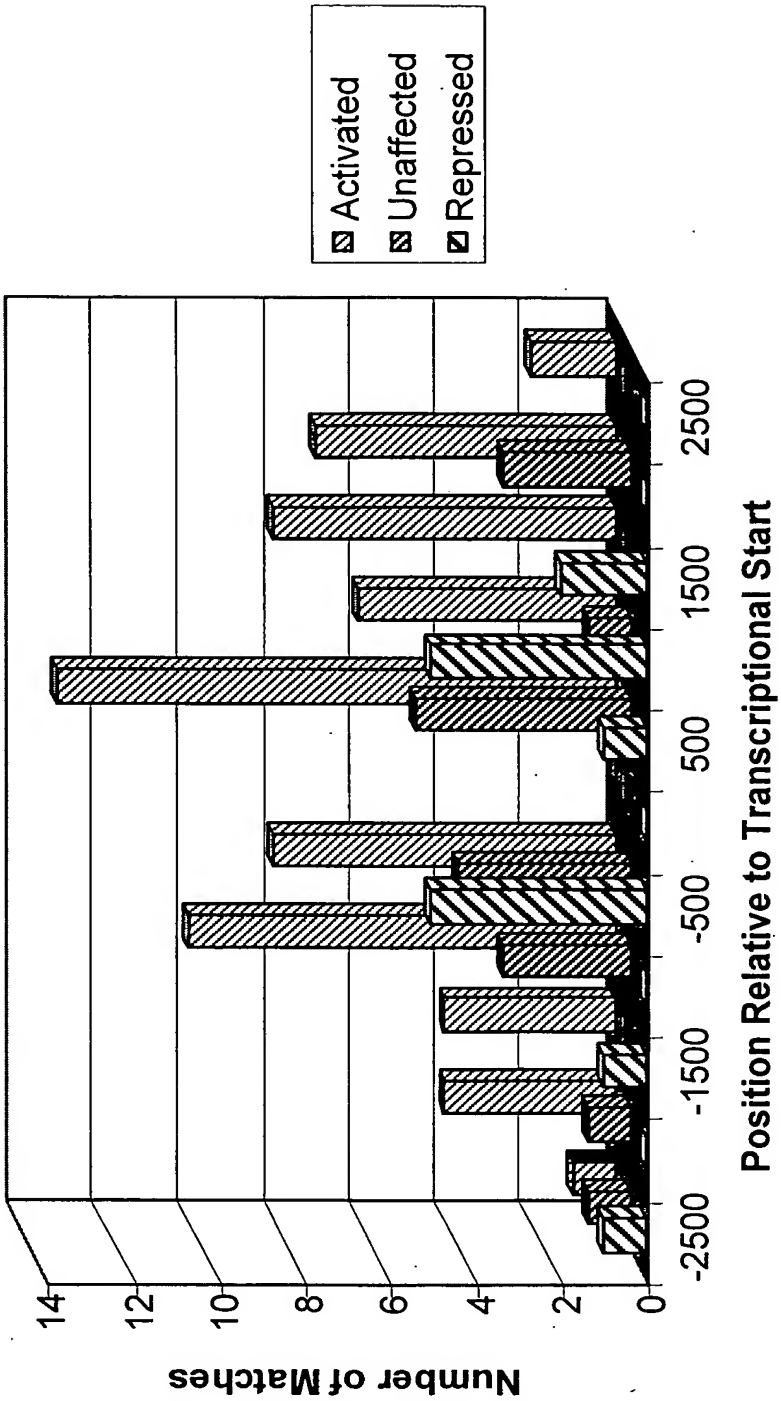

1
2
control
Target DNA sequences
Selected NRSF variants
Stable cell lines
Microarrays

FIG. 18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Unaffected
Repressed
Number of Matches
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2
4
6
8
10
12
14
-2500
-1500
-500
500
1500
2500
Position Relative to Transcriptional Start

FIG. 19

F4v1 (sequence identical to F4v2, F4v3)

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
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CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSD**HKTRYME**HVRTHTGERPYKCELCPYSSSQKTHLT
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
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GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 20

F4v4

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDHRTRYMEHVRTHTGERPYKCELCPYSSSQKTHLT
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
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KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 21

F4v5

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSD**HKTRYKE**HVRTHTGERPYKCELCPYSSSQKTHLT
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
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MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 22

F4v6

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
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RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
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GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 23

F4v7

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSD**HKTRYAE**HVRTHTGERPYKCELCPYSSSQKTHLT
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
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GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 24

F4v8

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
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KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
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GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
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FIG. 25

F5V1

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**TVGTLR**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
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GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 26

F5v2

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**TRGTLK**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 27

F5v3

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**TGSTLR**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 28

F5v4

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**TMSGLR**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 29

F5v5

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**TISALR**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 30

F5v6

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**HMPTLR**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 31

F5v7

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**HRGTLV**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 32

F5v8

MATQVMGQSSGGGGLFTSSGNIGMALPNDMYDLHDLSKAELAAPQLIMLANVALTGEVNGSCCDYLVGEERQMAELMPVG
DNNFSDSEEGEGLEESADIKGEPHGLENMELRSLELSVVEPQPVFEASGAPDIYSSNKDLPPETPGAEDKGKSSKTKPFR
CKPCQYEAESEEQFVHHIRVHSAKKFFVEESAEKQAKARESGSSTAEEGDFSKGPIRCDRCGYNTNRYDHYTAHLKHHTR
AGDNERVYKCIICTYTTVSEYHWRKHLRNHFPRKVYTCGKCNYFSDRKNNYVQHVRTHTGERPYKCELCPYSSS**RAPDLK**
RHMRTHSGEKPFKCDQCSYVASNQHEVTRHARQVHNGPKPLNCPHCDYKTADRSNFKKHVELHVNPRQFNCPVCDYAASK
KCNLQYHFKSKHPTCPNKTMDVSKVKLKKTKKREADLPDNITNEKTEIEQTKIKGDVAGKKNEKSVKAEKRDVSKEKKPS
NNVSVIQVTTRTRKSVTEVKEMDVHTGSNSEKFSKTKKSKRKLEVDSHSLHGPVNDEESSTKKKKKVESKSKNNSQEVPK
GDSKVEENKKQNTCMKKSTKKKTLKNKSSKKSSKPPQKEPVEKGSAQMDPPQMGPAPTEAVQKGPVQVELPPPMEHAQME
GAQIRPAPDEPVQMEVVQEGPAQKELLPPVEPAQMVGAQIVLAHMELPPPMETAQTEVAQMGPAPMEPAQMEVAQVESAP
MQVVQKEPVQMELSPPMEVVQKEPVQIELSPPMEVVQKEPVKIELSPPIEVVQKEPVQMELSPPMGVVQKEPAQREPPPP
REPPLHMEPISKKPPLRKDKKEKSNMQSERARKEQVLIEVGLVPVKDSWLLKESVSTEDLSPPSPPLPKENLREEASGDQ
KLLNTGEGNKEAPLQKVGAEEADESLPGLAANINESTHISSSGQNLNTPEGETLNGKHQTDSIVCEMKMDTDQNTRENLT
GINSTVEEPVSPMLPPSAVEEREAVSKTALASPPATMAANESQEIDEDEGIHSHEGSDLSDNMSEGSDDSGLHGARPVPQ
ESSRKNAKEALAVKAAKGDFVCIFCDRSFRKGKDYSKHLNRHLVNVYYLEEAAQGQE

FIG. 33

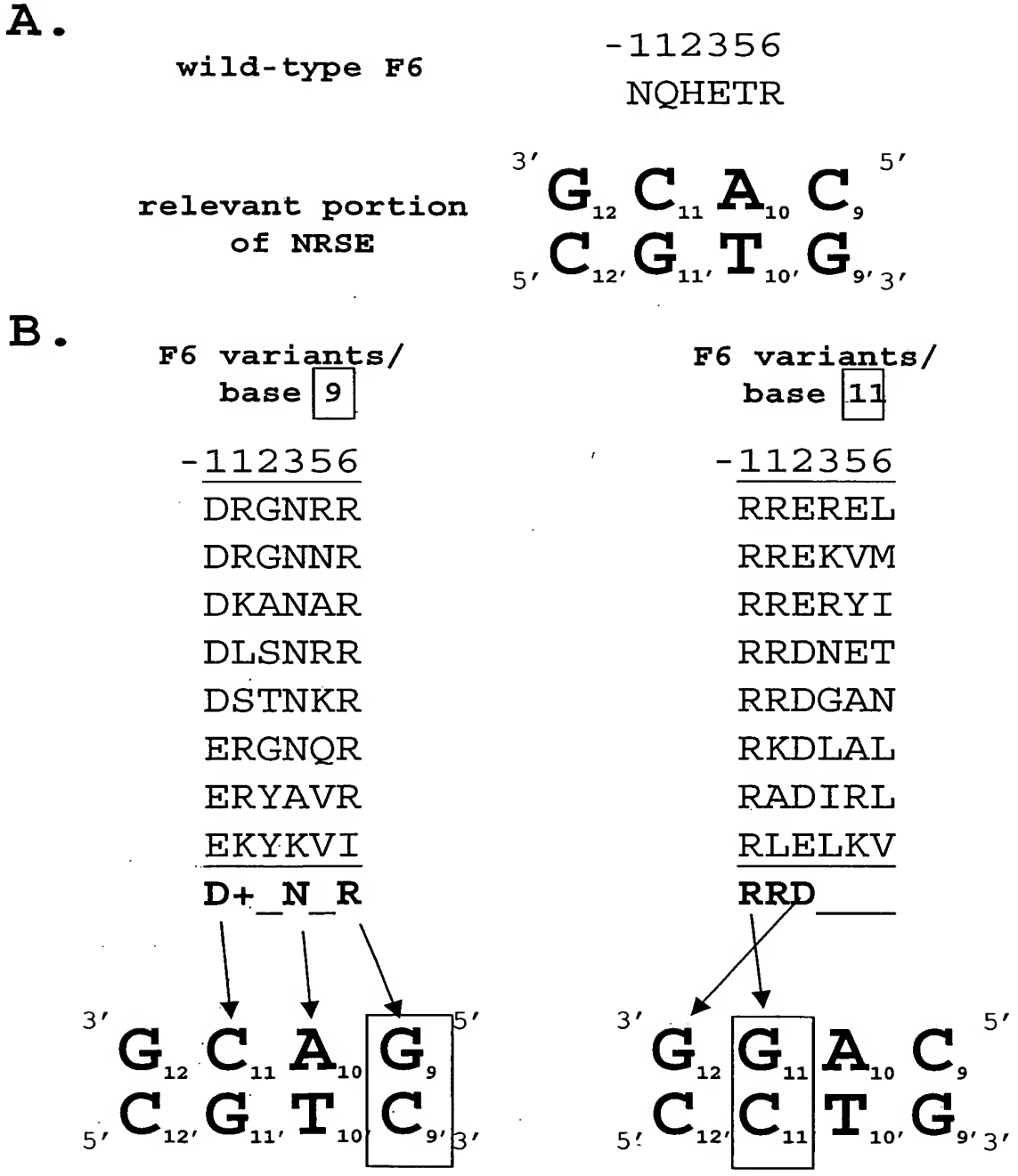
A.
wild-type F6
-112356
NQHETR
relevant portion of NRSE
3′ G12 C11 A10 C9 5′
5′ C12′ G11′ T10′ G9′ 3′
B.
F6 variants/ base 9
-112356
DRGNRR
DRGNNR
DKANAR
DLSNRR
DSTNKR
ERGNQR
ERYAVR
EKYKVI
D+_N_R
3′ G12 C11 A10 G9 5′
5′ C12′ G11′ T10′ C9′ 3′
F6 variants/ base 11
-112356
RREREL
RREKVM
RRERYI
RRDNET
RRDGAN
RKDLAL
RADIRL
RLELKV
RRD___
3′ G12 G11 A10 C9 5′
5′ C12′ C11 T10′ G9′ 3′

FIG. 34

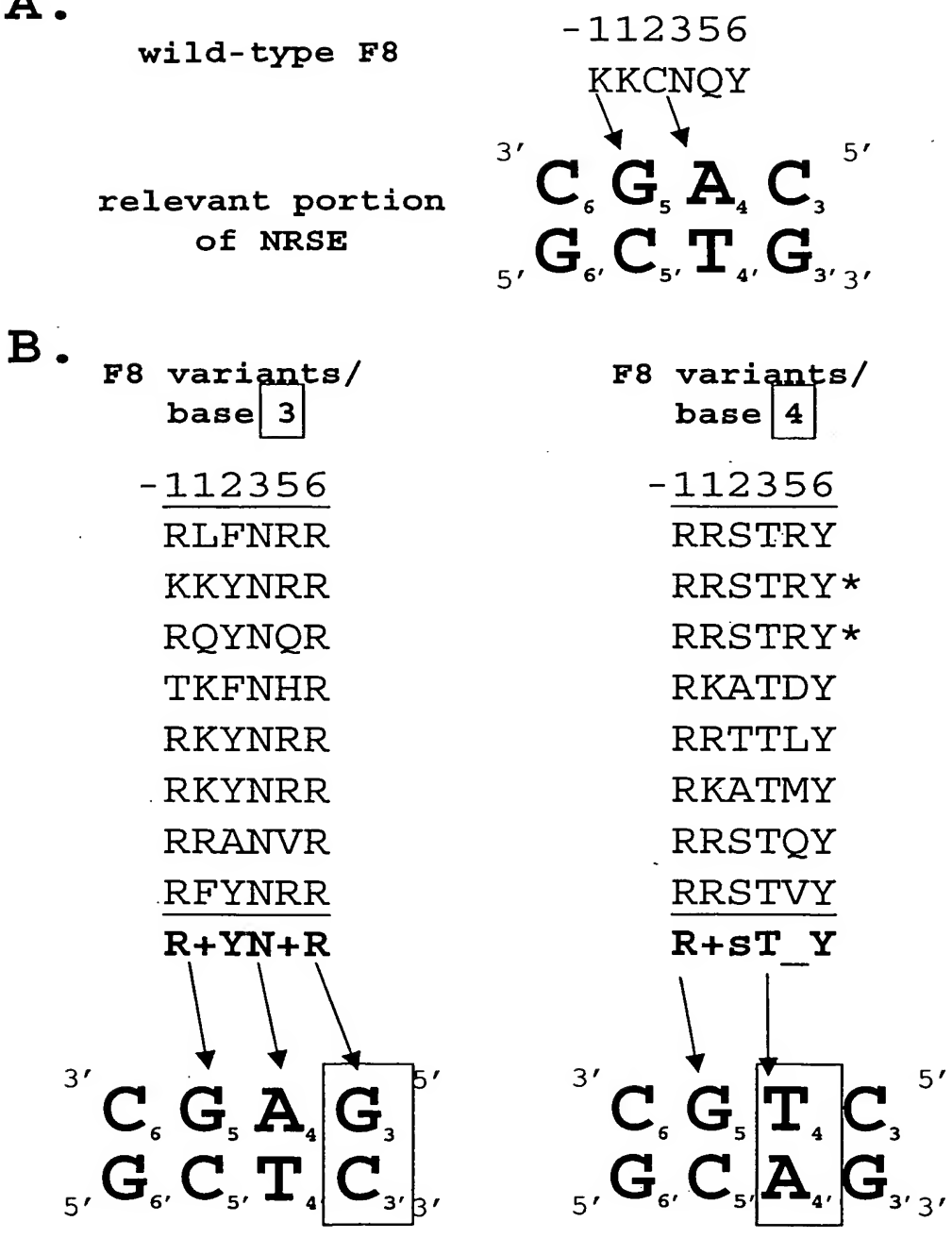
A.
wild-type F8
-112356
KKCNQY
relevant portion of NRSE
3′ C6 G5 A4 C3 5′
5′ G6′ C5′ T4′ G3′ 3′
B.
F8 variants/ base 3
-112356
RLFNRR
KKYNRR
RQYNQR
TKFNHR
RKYNRR
RKYNRR
RRANVR
RFYNRR
R+YN+R
3′ C6 G5 A4 G3 5′
5′ G6′ C5′ T4′ C3′ 3′
F8 variants/ base 4
-112356
RRSTRY
RRSTRY*
RRSTRY*
RKATDY
RRTTLY
RKATMY
RRSTQY
RRSTVY
R+sT_Y
3′ C6 G5 T4 C3 5′
5′ G6′ C5′ A4′ G3′ 3′

FIG. 35